

RAW SEQUENCE LISTING

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Application Serial Number: 10/538,922
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DATE: 08/14/2006

PATENT APPLICATION: US/10/538,922

TIME: 13:35:18

Input Set : A:\10-538,922 Sequence Listing.TXT

Output Set: N:\CRF4\08142006\J538922.raw

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3 <110> APPLICANT: CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
5 <120> TITLE OF INVENTION: METHOD OF DIAGNOSIS OF OBESITY
7 <130> FILE REFERENCE: Q88618
9 <140> CURRENT APPLICATION NUMBER: US 10/538,922
10 <141> CURRENT FILING DATE: 2005-06-13
12 <150> PRIOR APPLICATION NUMBER: EP 02 293 085
13 <151> PRIOR FILING DATE: 2002-12-13
15 <160> NUMBER OF SEQ ID NOS: 15
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1758
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <223> OTHER INFORMATION: gad2 gene
27 <400> SEQUENCE: 1
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29 gagaatcccg gcacagcgcg agcctggtgc caagtggctc agaagttcac gggcggcatc 120
30 ggaaacaaac tgtgcgccct gctctacgga gacgccgaga agccggcgga gagcggcggg 180
31 agccaacccc cgcgggccgc cgcccgaag gccgctgcg cctgcgacca gaagccctgc 240
32 agctgctcca aagtggatgt caactacgcg tttctccatg caacagacct gctgccggcg 300
33 tgtgatggag aaaggcccac tttggcgttt ctgcaagatg ttatgaacat tttacttcag 360
34 tatgtggtga aaagtttcga tagatcaacc aaagtgattg atttccatta tcctaattgag 420
35 cttctccaag aatataattg ggaattggca gaccaaccac aaaatttggg ggaaattttg 480
36 atgcattgcc aaacaactct aaaatatgca attaaaacag ggcattcctag atacttcaat 540
37 caactttcta ctggtttgga tatggttgga ttagcagcag actggctgac atcaacagca 600
38 aatactaaca tgttcacctg tgaaattgct ccagtatttg tgcttttgga atatgtcaca 660
39 ctaaagaaaa tgagagaaat cattggctgg ccagggggct ctggcgatgg gatattttct 720
40 cccggtggcg ccatatctaa catgtatgcc atgatgatcg cacgctttaa gatgttccca 780
41 gaagtcaagg agaaaggaat ggctgctctt cccaggctca ttgccttcac gtctgaacat 840
42 agtcattttt ctctcaagaa gggagctgca gccttaggga ttggaacaga cagcgtgatt 900
43 ctgattaaat gtgatgagag agggaaaatg attccatctg atcttgaaag aaggattctt 960
44 gaagccaaac agaaaggggt tgttcctttc ctcgtgagtg ccacagctgg aaccaccgtg 1020
45 tacggagcat ttgacccctt cttagctgtc gctgacattt gcaaaaagta taagatctgg 1080
46 atgcatgtgg atgcagcttg gggtagggga ttactgatgt cccgaaaaca caagtggaaa 1140
47 ctgagtggcg tggagagggc caactctgtg acgtggaatc cacacaagat gatgggagtc 1200
48 cctttgcagt gctctgctct cctgggttaga gaagagggat tgatgcagaa ttgcaaccaa 1260
49 atgcatgcct cctacctctt tcagcaagat aaacattatg acctgtccta tgacactgga 1320
50 gacaaggcct tacagtgcgg acgccacgtt gatgttttta aactatggct gatgtggagg 1380
51 gcaaagggga ctaccgggtt tgaagcgcat gttgataaat gtttggagtt ggcagagtat 1440
52 ttatacaaca tcataaaaaa ccgagaagga tatgagatgg tgtttgatgg gaagcctcag 1500
53 cacacaaatg tctgcttctg gtacattcct ccaagcttgc gtactctgga agacaatgaa 1560
54 gagagaatga gtcgcctctc gaaggtggct ccagtgatta aagccagaat gatggagtat 1620

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55 ggaaccacaa tggctagcta ccaacccttg ggagacaagg tcaatttctt ccgcatgggc 1680
56 atctcaaacc cagcggcaac tcaccaagac attgacttcc tgattgaaga aatagaacgc 1740
57 cttggacaag atttataa                                1758
60 <210> SEQ ID NO: 2
61 <211> LENGTH: 2382
62 <212> TYPE: DNA
63 <213> ORGANISM: Homo sapiens
65 <220> FEATURE:
66 <223> OTHER INFORMATION: 5' flanking region of gad2 gene nucleotides
68 <220> FEATURE:
69 <223> OTHER INFORMATION: R = G or A
71 <220> FEATURE:
72 <223> OTHER INFORMATION: Y = T or C
74 <220> FEATURE:
75 <223> OTHER INFORMATION: M = A or C
77 <220> FEATURE:
78 <223> OTHER INFORMATION: W = A or T
80 <220> FEATURE:
81 <223> OTHER INFORMATION: S = G or C
83 <400> SEQUENCE: 2
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85 gattttaaacg cttgctttta agaacccttta tgttttcaac cactcatcca tagtagaaaa 120
86 gttctgcaac cctagactgc tggcttgaag gaaaaccttt gcaggatttg atatggattt 180
87 caacaaagaa ccagcctctg cgaggctgga gagagctgcg gagctgccat gcctgaagtg 240
88 cagatggctg aaccacaagt ctttaggttt cgggagttgt tattgtggtg acctagagtg 300
89 tcagagccag gagagcaaga aagaggagcc aaactgagcc ctgagttttc gaccaccggy 360
90 gctccacacg cctggwacag acttcaccta gcacgctcag tgccagcctt cggcaggacg 420
91 ctatcaacgc ccgactggwt tcytgctctc atcctggcgc ctgggcccag ttgccatagt 480
92 gtggatccca tgactcctca gggaaacccct ggactcaggc acgcgagaag aagacagcgc 540
93 tttgtggaga gaattgacca gggacagtta tgctcgagca cacaggactt gggcctgtat 600
94 gcgtccagca tgggccccag gatgtccctt ctaagcgagg gtcgaggggt gctcgcccag 660
95 acgggatccc cgggtctctg ctttgtagc agctttggtg gctggttcag gaggtcagag 720
96 aaataaaacg acttgtgaac acaatggaaa tgacaggcgc tctggccagg cgcggggaar 780
97 gcagccgcct cgggaagcgc acctcagccc ttctctctct ctccctccct ccgtctcccc 840
98 cagagccccg gagctccgag gtgcacttga agttcatctc cactgccagg agaacgcagc 900
99 gcaaaactgtc aaaggggctcc caatccttag ggcgtcctcc ctgtctgcaa tagctttttg 960
100 tagaaaggaa atcatcagaa mgattctgac tttctcctcc tttctttatt agaaaaagag 1020
101 aaaccgcctc ctaatacgcc tcagagagaa ccaatctcgc gcttcggggt caccgcgtac 1080
102 cgcgaagatt ctctgggggc gagggggggc attggtttga agccccctaa aacgagggcc 1140
103 ctgcaggcga tgccctcttt cctactcgga ttgttaaagc cgagattgct tagttggaaa 1200
104 cctgtttctc cctcccagg cgcacacaga tcccccttac acgcaagcag cgggcgcttc 1260
105 cagcctccg cgggccaagg tcaccaaagt ccctgattcc atccccacc cgccatcaat 1320
106 cctgcgcact ctggccgctc tgccctattc tcttccaaga agtttccatt cgttttattt 1380
107 ttttttcccc agcccagagt cctcagtaga ctccagcgtg gattttaatt gcctcaatca 1440
108 gcagtcattc tccccagccg tcaactcagag cctggacggg ggggtcccgc atctagccct 1500
109 tggttacgca ggaacggtgc gccccgggg acggcgcggt tcagcaggca ggcgtcaggt 1560
110 tctaccaagg cgctgaaatg agcccatcag cgggtaggag cccttcccc gccgtccct 1620
111 cccaggtc gtgaacggcg cctgatgccc gcccgggcg cgagctctcg aggtcgcagt 1680
112 gacctcagca cctgcttggg ggaacacggc gcgggaaccc cgcttccttc ccctcagctg 1740

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113 gagccagacc tcaaacaaaa ccccaatcga tgcacacaga aaactcctct gggccacgct 1800
114 tcccgccctcg ccgaggtctc cccagtctgc ccctcgctga cgctggcgcg cagcsgctgt 1860
115 ggcagcaccc gggacagcgg ccgcccgcac ttcccgctc tggctcgccc gaggacgcgc 1920
116 tggcagcgct cccacccct cactctgact ccagctggcg tgcattggtct gcctcgcatc 1980
117 ctacagactc agctccctcc ctctctcgctg ttttttctc ccgcgcgcc ctcattcatc 2040
118 cccactgggc tccctttccc tcaaagtctc tggggctctc cgcgctttcc tgagtccggg 2100
119 ctccgaggac ccttaggtag tcccggtctc ttttaargct ccccggttcc caaagggttg 2160
120 ccacgtccct aaacctgtc tccagctcgc atacacacac gcacagacac gcacgttttc 2220
121 tgttcctgcg tgacacccgc cctcgccgct cggccccgcc ggtccccgcg cggcgccctc 2280
122 ctcccgccac acgggcacgc acgcgcgcgc agggccaagc ccgaggcagc tcgcccgcag 2340
123 ctgcactcg caggcgacct gctccagtct ccaaagccga tg 2382
126 <210> SEQ ID NO: 3
127 <211> LENGTH: 519
128 <212> TYPE: PRT
129 <213> ORGANISM: Homo sapiens
131 <220> FEATURE:
132 <223> OTHER INFORMATION: DNA-binding protein Ikaros (Lymphoid transcription factor
133 LyF-1)
135 <400> SEQUENCE: 3
136 Met Asp Ala Asp Glu Gly Gln Asp Met Ser Gln Val Ser Gly Lys Glu
137 1 5 10 15
139 Ser Pro Pro Val Ser Asp Thr Pro Asp Glu Gly Asp Glu Pro Met Pro
140 20 25 30
142 Ile Pro Glu Asp Leu Ser Thr Thr Ser Gly Gly Gln Gln Ser Ser Lys
143 35 40 45
145 Ser Asp Arg Val Val Ala Ser Asn Val Lys Val Glu Thr Gln Ser Asp
146 50 55 60
148 Glu Glu Asn Gly Arg Ala Cys Glu Met Asn Gly Glu Glu Cys Ala Glu
149 65 70 75 80
151 Asp Leu Arg Met Leu Asp Ala Ser Gly Glu Lys Met Asn Gly Ser His
152 85 90 95
154 Arg Asp Gln Gly Ser Ser Ala Leu Ser Gly Val Gly Gly Ile Arg Leu
155 100 105 110
157 Pro Asn Gly Lys Leu Lys Cys Asp Ile Cys Gly Ile Ile Cys Ile Gly
158 115 120 125
160 Pro Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Glu Arg Pro
161 130 135 140
163 Phe Gln Cys Asn Gln Cys Gly Ala Ser Phe Thr Gln Lys Gly Asn Leu
164 145 150 155 160
166 Leu Arg His Ile Lys Leu His Ser Gly Glu Lys Pro Phe Lys Cys His
167 165 170 175
169 Leu Cys Asn Tyr Ala Cys Arg Arg Arg Asp Ala Leu Thr Gly His Leu
170 180 185 190
172 Arg Thr His Ser Val Gly Lys Pro His Lys Cys Gly Tyr Cys Gly Arg
173 195 200 205
175 Ser Tyr Lys Gln Arg Ser Ser Leu Glu Glu His Lys Glu Arg Cys His
176 210 215 220
178 Asn Tyr Leu Glu Ser Met Gly Leu Pro Gly Thr Leu Tyr Pro Val Ile
179 225 230 235 240

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181 Lys Glu Glu Thr Asn His Ser Glu Met Ala Glu Asp Leu Cys Lys Ile
182                               245                               250                               255
184 Gly Ser Glu Arg Ser Leu Val Leu Asp Arg Leu Ala Ser Asn Val Ala
185                               260                               265                               270
187 Lys Arg Lys Ser Ser Met Pro Gln Lys Phe Leu Gly Asp Lys Gly Leu
188                               275                               280                               285
190 Ser Asp Thr Pro Tyr Asp Ser Ser Ala Ser Tyr Glu Lys Glu Asn Glu
191                               290                               295                               300
193 Met Met Lys Ser His Val Met Asp Gln Ala Ile Asn Asn Ala Ile Asn
194 305                               310                               315                               320
196 Tyr Leu Gly Ala Glu Ser Leu Arg Pro Leu Val Gln Thr Pro Pro Gly
197                               325                               330                               335
199 Gly Ser Glu Val Val Pro Val Ile Ser Pro Met Tyr Gln Leu His Lys
200                               340                               345                               350
202 Pro Leu Ala Glu Gly Thr Pro Arg Ser Asn His Ser Ala Gln Asp Ser
203                               355                               360                               365
205 Ala Val Glu Asn Leu Leu Leu Ser Lys Ala Lys Leu Val Pro Ser
206                               370                               375                               380
208 Glu Arg Glu Ala Ser Pro Ser Asn Ser Cys Gln Asp Ser Thr Asp Thr
209 385                               390                               395                               400
211 Glu Ser Asn Asn Glu Glu Gln Arg Ser Gly Leu Ile Tyr Leu Thr Asn
212                               405                               410                               415
214 His Ile Ala Pro His Ala Arg Asn Gly Leu Ser Leu Lys Glu Glu His
215                               420                               425                               430
217 Arg Ala Tyr Asp Leu Leu Arg Ala Ala Ser Glu Asn Ser Gln Asp Ala
218                               435                               440                               445
220 Leu Arg Val Val Ser Thr Ser Gly Glu Gln Met Lys Val Tyr Lys Cys
221                               450                               455                               460
223 Glu His Cys Arg Val Leu Phe Leu Asp His Val Met Tyr Thr Ile His
224 465                               470                               475                               480
226 Met Gly Cys His Gly Phe Arg Asp Pro Phe Glu Cys Asn Met Cys Gly
227                               485                               490                               495
229 Tyr His Ser Gln Asp Arg Tyr Glu Phe Ser Ser His Ile Thr Arg Gly
230                               500                               505                               510
232 Glu His Arg Phe His Met Ser
233                               515
236 <210> SEQ ID NO: 4
237 <211> LENGTH: 20
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: Chemically synthesized Primer to amplify SNP - 243
244 <400> SEQUENCE: 4
245 cctcaaagtc tctggggctc                                     20
248 <210> SEQ ID NO: 5
249 <211> LENGTH: 20
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:

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254 <223> OTHER INFORMATION: Chemically synthesized Primer to amplify SNP - 243
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 257 ggtgtcacgc aggaacagaa 20
 260 <210> SEQ ID NO: 6
 261 <211> LENGTH: 23
 262 <212> TYPE: DNA
 263 <213> ORGANISM: Artificial Sequence
 265 <220> FEATURE:
 266 <223> OTHER INFORMATION: Chemically synthesized Primer to amplify SNP - 243
 268 <400> SEQUENCE: 6
 269 gtctctttta aagctccccg gct 23
 272 <210> SEQ ID NO: 7
 273 <211> LENGTH: 28
 274 <212> TYPE: DNA
 275 <213> ORGANISM: Artificial Sequence
 277 <220> FEATURE:
 278 <223> OTHER INFORMATION: Chemically synthesized Primer to amplify SNP - 243
 280 <400> SEQUENCE: 7
 281 cgggctccga ggacccttag gtagtccc 28
 285 <210> SEQ ID NO: 8
 286 <211> LENGTH: 17
 287 <212> TYPE: DNA
 288 <213> ORGANISM: Artificial Sequence
 290 <220> FEATURE:
 291 <223> OTHER INFORMATION: Chemically synthesized Primer to amplify SNP - 1.6 kb
 293 <400> SEQUENCE: 8
 294 ctgaggcgta ttaggag 17
 297 <210> SEQ ID NO: 9
 298 <211> LENGTH: 17
 299 <212> TYPE: DNA
 300 <213> ORGANISM: Artificial Sequence
 302 <220> FEATURE:
 303 <223> OTHER INFORMATION: Chemically synthesized Primer to amplify SNP - 1.6 kb
 305 <400> SEQUENCE: 9
 306 ctccctaatac gcctcag 17
 309 <210> SEQ ID NO: 10
 310 <211> LENGTH: 16
 311 <212> TYPE: DNA
 312 <213> ORGANISM: Artificial Sequence
 314 <220> FEATURE:
 315 <223> OTHER INFORMATION: Chemically synthesized Primer to amplify SNP - 1.6 kb
 317 <400> SEQUENCE: 10
 318 ggaaagcagc cgcctc 16
 321 <210> SEQ ID NO: 11
 322 <211> LENGTH: 30
 323 <212> TYPE: DNA
 324 <213> ORGANISM: Artificial Sequence
 326 <220> FEATURE:
 327 <223> OTHER INFORMATION: Chemically synthesized Primer to amplify SNP - 1.6 kb

VERIFICATION SUMMARY

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